RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/038,722B_

Source: _1FW16_

Date Processed by STIC: _4/21/05_

ENTERED

RAW SEQUENCE LISTING   DATE: 04/21/2005
PATENT APPLICATION: US/10/038,722B   TIME: 11:42:03

     Input Set : A:\D0617.70005US01 seqs.txt
     Output Set: N:\CRF4\04212005\J038722B.raw

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 4 <110> APPLICANT: LEY, Arthur C.
 5        GUTERMAN, Sonia K.
 6        MARKLAND, William
 7        KENT, Rachel B.
 8        ROBERTS, Bruce L.
 9        LADNER, Robert C.
11 <120> TITLE OF INVENTION: ITI-D1 KUNITZ DOMAIN MUTANTS AS HNE INHIBITORS
13 <130> FILE REFERENCE: D0617.7005US01
15 <140> CURRENT APPLICATION NUMBER: 10/038,722B
16 <141> CURRENT FILING DATE: 2002-01-08
18 <150> PRIOR APPLICATION NUMBER: US 08/849,406
19 <151> PRIOR FILING DATE: 1999-07-21
21 <150> PRIOR APPLICATION NUMBER: PCT/US95/16349
22 <151> PRIOR FILING DATE: 1995-12-15
24 <150> PRIOR APPLICATION NUMBER: US 08/358,160
25 <151> PRIOR FILING DATE: 1994-12-16
27 <150> PRIOR APPLICATION NUMBER: US 08/133,031
28 <151> PRIOR FILING DATE: 1992-02-28
30 <160> NUMBER OF SEQ ID NOS: 143
32 <170> SOFTWARE: PatentIn version 3.1
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36 <211> LENGTH: 276
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
40 <220> FEATURE:
42 <223> OTHER INFORMATION: IIIsp::bpti::matureIII (initial fragment)
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45 gtgaaaaaat tattattcgc aattccttta gttgttcctt tctattctgg cgcccgtccg       60
47 gatttctgtc tcgagccacc atacactggg ccctgcaaag cgcgcatcat ccgctatttc      120
49 tacaatgcta aagcaggcct gtgccagacc tttgtatacg gtggttgccg tgctaagcgt      180
51 aacaacttta aatcggccga agattgcatg cgtacctgcg gtggcgccgc tgaaactgtt      240
53 gaaagttgtt tagcaaaacc ccatacagaa aattca                               276
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57 <211> LENGTH: 92
58 <212> TYPE: PRT
59 <213> ORGANISM: Artificial Sequence
61 <220> FEATURE:
62 <223> OTHER INFORMATION: IIIsp::bpti::matureIII (initial fragment)
64 <400> SEQUENCE: 2
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67 1               5                   10                  15
69 Gly Ala Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys
70             20                  25                  30
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72 Lys Ala Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys
73         35              40              45
75 Gln Thr Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys
76     50              55              60
78 Ser Ala Glu Asp Cys Met Arg Thr Cys Gly Gly Ala Ala Glu Thr Val
79 65              70              75              80
81 Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser
82             85              90
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86 <211> LENGTH: 285
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
92 <223> OTHER INFORMATION: IIIsp::itiD1::mature III fusion gene
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97 gactcttgcc agctgggcta ctcggccggt ccctgcatgg gaatgaccag caggtatttc     120
99 tataatggta catccatggc ctgtgagact ttccagtacg gcggctgcat gggcaacggt     180
101 aacaacttcg tcacagaaaa ggagtgtctg cagacctgcc gaactgtggg cgccgctgaa     240
103 actgttgaaa gttgtttagc aaaaccccat acagaaaatt cattt                     285
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107 <211> LENGTH: 95
108 <212> TYPE: PRT
109 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
113 <223> OTHER INFORMATION: IIIsp::itiD1::mature III fusion gene
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118 1             5              10              15
120 Gly Ala Lys Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys
121         20              25              30
123 Met Gly Met Thr Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys
124         35              40              45
126 Glu Thr Phe Gln Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Val
127     50              55              60
129 Thr Glu Lys Glu Cys Leu Gln Thr Cys Arg Thr Val Gly Ala Ala Glu
130 65              70              75              80
132 Thr Val Glu Ser Cys Leu Ala Lys Pro His Thr Glu Asn Ser Phe
133             85              90              95
136 <210> SEQ ID NO: 5
137 <211> LENGTH: 58
138 <212> TYPE: PRT
139 <213> ORGANISM: Artificial Sequence
141 <220> FEATURE:
143 <223> OTHER INFORMATION: Consensus Kunitz domain
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148 1             5              10              15
150 Met Ile Pro Arg Phe Tyr Tyr Asn Ala Lys Ser Gly Lys Cys Glu Pro
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151            20              25              30
153 Phe Ile Tyr Gly Gly Cys Gly Gly Asn Ala Asn Asn Phe Lys Thr Glu
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156 Glu Glu Cys Arg Arg Thr Cys Gly Gly Ala
157    50              55
160 <210> SEQ ID NO: 6
161 <211> LENGTH: 58
162 <212> TYPE: PRT
163 <213> ORGANISM: Bos Taurus
165 <400> SEQUENCE: 6
167 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Lys Ala
168 1           5              10              15
170 Arg Ile Ile Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
171         20              25              30
174 Phe Val Tyr Gly Gly Cys Arg Ala Lys Arg Asn Asn Phe Lys Ser Ala
175         35              40              45
177 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
178    50              55
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182 <211> LENGTH: 58
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
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187 <223> OTHER INFORMATION: Epi-HNE-1
189 <400> SEQUENCE: 7
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192 1           5              10              15
194 Phe Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
195         20              25              30
197 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
198         35              40              45
200 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
201    50              55
204 <210> SEQ ID NO: 8
205 <211> LENGTH: 62
206 <212> TYPE: PRT
207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
211 <223> OTHER INFORMATION: Epi-HNE-2
213 <400> SEQUENCE: 8
215 Glu Ala Glu Ala Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly
216 1           5              10              15
218 Pro Cys Ile Ala Phe Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly
219         20              25              30
221 Leu Cys Gln Thr Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn
222         35              40              45
224 Phe Lys Ser Ala Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
225    50              55              60
228 <210> SEQ ID NO: 9
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229 <211> LENGTH: 58
230 <212> TYPE: PRT
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
235 <223> OTHER INFORMATION: EpiNE7
237 <400> SEQUENCE: 9
239 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Ala
240 1   5   10   15
241 Met Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
242   20   25   30
244 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
245   35   40   45
246 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
247   50   55
250 <210> SEQ ID NO: 10
251 <211> LENGTH: 58
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
257 <223> OTHER INFORMATION: EpiNE3
259 <400> SEQUENCE: 10
261 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Gly
262 1   5   10   15
264 Phe Phe Ser Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
265   20   25   30
267 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
268   35   40   45
270 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
271   50   55
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275 <211> LENGTH: 58
276 <212> TYPE: PRT
277 <213> ORGANISM: Artificial Sequence
279 <220> FEATURE:
281 <223> OTHER INFORMATION: EpiNE6
283 <400> SEQUENCE: 11
285 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Gly
286 1   5   10   15
288 Phe Phe Gln Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
289   20   25   30
291 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
292   35   40   45
294 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
295   50   55
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300 <212> TYPE: PRT
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:

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307 <400> SEQUENCE: 12
309 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Ala
310 1               5                   10                  15
312 Ile Phe Pro Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
313             20                  25                  30
315 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
316         35                  40                  45
318 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
319     50                  55
322 <210> SEQ ID NO: 13
323 <211> LENGTH: 58
324 <212> TYPE: PRT
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
329 <223> OTHER INFORMATION: EpiNE8
331 <400> SEQUENCE: 13
333 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Val Ala
334 1               5                   10                  15
336 Phe Phe Lys Arg Ser Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
337             20                  25                  30
339 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
340         35                  40                  45
342 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
343     50                  55
346 <210> SEQ ID NO: 14
347 <211> LENGTH: 58
348 <212> TYPE: PRT
349 <213> ORGANISM: Artificial Sequence
351 <220> FEATURE:
353 <223> OTHER INFORMATION: EpiNE5
355 <400> SEQUENCE: 14
357 Arg Pro Asp Phe Cys Leu Glu Pro Pro Tyr Thr Gly Pro Cys Ile Ala
358 1               5                   10                  15
360 Phe Phe Gln Arg Tyr Phe Tyr Asn Ala Lys Ala Gly Leu Cys Gln Thr
361             20                  25                  30
362 Phe Val Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Lys Ser Ala
363         35                  40                  45
365 Glu Asp Cys Met Arg Thr Cys Gly Gly Ala
366     50                  55
368 <210> SEQ ID NO: 15
369 <211> LENGTH: 58
370 <212> TYPE: PRT
371 <213> ORGANISM: Artificial Sequence
373 <220> FEATURE:
375 <223> OTHER INFORMATION: EpiNE2
377 <400> SEQUENCE: 15
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380 1               5                   10                  15
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/21/2005
PATENT APPLICATION: US/10/038,722B   TIME: 11:42:04

Input Set : A:\D0617.70005US01 seqs.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:82; N Pos. 37,38,40,41,42,47,52,56,58,64,65,66,71,72,100,101,103,104
Seq#:82; N Pos. 109,110,124,125,128,133,134
Seq#:83; Xaa Pos. 13,14,16,18,19,20,22,24,34,35,37,42,43,45
Seq#:84; N Pos. 34,35,37,38,39,43,44,49,53,55,56,61,62,63,68,69,97,98,100
Seq#:84; N Pos. 101,106,107,121,122,125,130,131
Seq#:85; Xaa Pos. 12,13,15,17,18,19,21,23,33,34,36,41,42,44
Seq#:86; Xaa Pos. 2,3,4,5,6,7,9,11,12,13,14,15,16,17,18,19,20,21,22,23,24
Seq#:86; Xaa Pos. 25,27,28,30,31,32,35,36,37,38,39,40,41,42,43,44,45,46,48
Seq#:86; Xaa Pos. 49,50
Seq#:103; Xaa Pos. 1
Seq#:104; Xaa Pos. 1
Seq#:106; Xaa Pos. 1
Seq#:109; Xaa Pos. 1
Seq#:123; Xaa Pos. 1
Seq#:127; N Pos. 4,5,6,7,8
Seq#:128; N Pos. 4,5,6,7,8,9,10,11,12

VERIFICATION SUMMARY   DATE: 04/21/2005
PATENT APPLICATION: **US/10/038,722B**   TIME: 11:42:04

Input Set : **A:\D0617.70005US01 seqs.txt**
Output Set: **N:\CRF4\04212005\J038722B.raw**

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L:2331 M:283 W: Missing Blank Line separator, <400> field identifier
L:2807 M:283 W: Missing Blank Line separator, <220> field identifier
L:2923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:82 after pos.:0
M:341 Repeated in SeqNo=82
L:2991 M:283 W: Missing Blank Line separator, <220> field identifier
L:3013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0
M:341 Repeated in SeqNo=83
L:3064 M:283 W: Missing Blank Line separator, <220> field identifier
L:3165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:84 after pos.:0
M:341 Repeated in SeqNo=84
L:3257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85 after pos.:0
M:341 Repeated in SeqNo=85
L:3356 M:283 W: Missing Blank Line separator, <400> field identifier
L:3358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86 after pos.:0
M:341 Repeated in SeqNo=86
L:3743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:0
L:3768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:0
L:3816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0
L:3880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:109 after pos.:0
L:4177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:123 after pos.:0
L:4280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:127 after pos.:0
L:4298 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:128 after pos.:0
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